

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/530,884A

CRF Processing Date: 6/10/2002

Edited by: [Signature]

Verified by: [Signature] (STIC staff)

ENTERED

1646

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seqs 5,8,48-corrected amino acid numbering

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JUN 12 2002

TECH CENTER 1600/2900

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/530,884A

DATE: 06/10/2002

TIME: 19:54:37

Input Set : A:\PTO.AMC.TXT

Output Set: N:\CRF3\06102002\I530884A.raw

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JUN 12 2002

TECH CENTER 1600/2900

4 <110> APPLICANT: McBurney, Robert N.
5 Holt, William
6 Gwynne, David I.
7 Marchionni, Mark
9 <120> TITLE OF INVENTION: Therapeutic Methods Comprising Use of a
10 Neuregulin
12 <130> FILE REFERENCE: 04585/048002
14 <140> CURRENT APPLICATION NUMBER: US 09/530,884A
15 <141> CURRENT FILING DATE: 2000-08-29
17 <150> PRIOR APPLICATION NUMBER: PCT/US98/21349
18 <151> PRIOR FILING DATE: 1998-10-08
20 <150> PRIOR APPLICATION NUMBER: US 60/062,109
21 <151> PRIOR FILING DATE: 1997-10-14
23 <160> NUMBER OF SEQ ID NOS: 54
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 745
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)...(744)
36 <400> SEQUENCE: 1
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38 Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
39 1 5 10 15
41 gcc cag cgc ccc ggc tcc gcc gcc cgc tcg tcg ccg ccg ctg ccg ctg 96
42 Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
43 20 25 30
45 ctg cca cta ctg ctg ctg ctg ggg acc gcg gcc ctg gcg ccg ggg gcg 144
46 Leu Pro Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
47 35 40 45
49 gcg gcc gcc aac gag gcg gct ccc gcg ggg gcc tcg gtg tgc tac tcg 192
50 Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
51 50 55 60
53 tcc ccg ccc agc gtg gga tcg gtg cag gag cta gct cag cgc gcc gcg 240
54 Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
55 65 70 75 80
57 gtg gtg atc gag gga aag gtg cac ccg cag cgg cgg cag cag ggg gca 288
58 Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
59 85 90 95
61 ctg gac agg aag gcg gcg gcg gcg gcg ggc gag gca ggg gcg tgg ggc 336
62 Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly

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63          100          105          110
65 ggc gat cgc gag ccg cca gcc gcg ggc cca cgg gcg ctg ggg ccg ccc 384
66 Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
67          115          120          125
69 gcc gag gag ccg ctg ctc gcc gcc aac ggg acc gtg ccc tct tgg ccc 432
70 Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
71          130          135          140
73 acc gcc ccg gtg ccc agc gcc ggc gag ccc ggg gag gag gcg ccc tat 480
74 Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
75 145          150          155          160
77 ctg gtg aag gtg cac cag gtg tgg gcg gtg aaa gcc ggg ggc ttg aag 528
78 Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
79          165          170          175
81 aag gac tcg ctg ctc acc gtg cgc ctg ggg acc tgg ggc cac ccc gcc 576
82 Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
83          180          185          190
85 ttc ccc tcc tgc ggg agg ctc aag gag gac agc agg tac atc ttc ttc 624
86 Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
87          195          200          205
89 atg gag ccc gac gcc aac agc acc agc cgc gcg ccg gcc gcc ttc cga 672
90 Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
91          210          215          220
93 gcc tct ttc ccc cct ctg gag acg ggc cgg aac ctc aag aag gag gtc 720
94 Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
95 225          230          235          240
97 agc cgg gtg ctg tgc aag cgg tgc g 745
98 Ser Arg Val Leu Cys Lys Arg Cys
99          245
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 248
104 <212> TYPE: PRT
105 <213> ORGANISM: Homo sapiens
107 <400> SEQUENCE: 2
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109 1          5          10          15
110 Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
111          20          25          30
112 Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
113          35          40          45
114 Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
115          50          55          60
116 Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
117 65          70          75          80
118 Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
119          85          90          95
120 Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
121          100          105          110
122 Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
123          115          120          125
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Input Set : A:\PTO.AMC.TXT

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124 Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
125 130 135 140
126 Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
127 145 150 155 160
128 Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
129 165 170 175
130 Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
131 180 185 190
132 Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
133 195 200 205
134 Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
135 210 215 220
136 Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
137 225 230 235 240
138 Ser Arg Val Leu Cys Lys Arg Cys
139 245

142 <210> SEQ ID NO: 3

143 <211> LENGTH: 252

144 <212> TYPE: DNA

145 <213> ORGANISM: Bos taurus

147 <220> FEATURE:

148 <221> NAME/KEY: CDS

149 <222> LOCATION: (3)...(251)

151 <400> SEQUENCE: 3

152 cc cat caa gtg tgg gcg gcg aaa gcc ggg ggc ttg aag aag gac tgc 47
153 His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser
154 1 5 10 15
156 ctg ctc acc gtg cgc ctg ggc gcc tgg ggc cac ccc gcc ttc ccc tcc 95
157 Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
158 20 25 30
160 tgc ggg cgc ctc aag gag gac agc agg tac atc ttc ttc atg gag ccc 143
161 Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro
162 35 40 45
164 gag gcc aac agc agc ggc ggg ccc ggc cgc ctt ccg agc ctc ctt ccc 191
165 Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro
166 50 55 60
168 ccc tct cga gac ggg ccg gaa cct caa gaa gga ggt cag ccg ggt gct 239
169 Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala
170 65 70 75
172 gtg caa cgg tgc g 252
173 Val Gln Arg Cys
174 80
177 <210> SEQ ID NO: 4
178 <211> LENGTH: 83
179 <212> TYPE: PRT
180 <213> ORGANISM: Bos taurus
182 <400> SEQUENCE: 4
183 His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
184 1 5 10 15

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185 Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
186          20          25          30
187 Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
188          35          40          45
189 Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
190          50          55          60
191 Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
192 65          70          75          80
193 Gln Arg Cys
197 <210> SEQ ID NO: 5
198 <211> LENGTH: 59
199 <212> TYPE: PRT
200 <213> ORGANISM: Bos taurus
202 <400> SEQUENCE: 5
203 Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Val Ala Gly
204 1          5          10          15
205 Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
206          20          25          30
207 Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
208          35          40          45
209 Pro Gln Asn Ile Lys Ile Gln Lys Arg Pro Gly
210          50          55
213 <210> SEQ ID NO: 6
214 <211> LENGTH: 178
215 <212> TYPE: DNA
216 <213> ORGANISM: Bos taurus
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (3)...(176)
222 <400> SEQUENCE: 6
223 cc ttg cct ccc cgc ttg aaa gag atg aag agt cag gag tct gtg gca 47
224 Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Val Ala
225 1          5          10          15
227 ggt tcc aaa cta gtg ctt cgg tgc gag acc agt tct gaa tac tcc tct 95
228 Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser
229          20          25          30
231 ctc aag ttc aag tgg ttc aag aat ggg agt gaa tta agc cga aag aac 143
232 Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn
233          35          40          45
235 aaa cca caa aac atc aag ata cag aaa agg ccg gg 178
236 Lys Pro Gln Asn Ile Lys Ile Gln Lys Arg Pro
237          50          55
240 <210> SEQ ID NO: 7
241 <211> LENGTH: 178
242 <212> TYPE: DNA
243 <213> ORGANISM: Homo sapiens
245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (1)...(177)

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,884A

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Input Set : A:\PTO.AMC.TXT
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249 <400> SEQUENCE: 7
250 cct tgc ctc ccc gat tga aag aga tga aaa gcc agg aat cgg ctg cag 48
251 Pro Cys Leu Pro Asp * Lys Arg * Lys Ala Arg Asn Arg Leu Gln
252 1 5 10
254 gtt cca aac tag tcc ttc ggt gtg aaa cca gtt ctg aat act cct ctc 96
255 Val Pro Asn * Ser Phe Gly Val Lys Pro Val Leu Asn Thr Pro Leu
256 15 20 25
258 tca gat tca agt ggt tca aga atg gga atg aat tga atc gaa aaa aca 144
259 Ser Asp Ser Ser Gly Ser Arg Met Gly Met Asn * Ile Glu Lys Thr
260 30 35 40
262 aac cac aaa ata tca aga tac aaa aaa agc cag g 178
263 Asn His Lys Ile Ser Arg Tyr Lys Lys Ser Gln
264 45 50 55
267 <210> SEQ ID NO: 8
268 <211> LENGTH: 59
269 <212> TYPE: PRT
270 <213> ORGANISM: Homo sapiens
272 <400> SEQUENCE: 8
273 Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly
274 1 5 10 15
275 Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
276 20 25 30
277 Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys
278 35 40 45
279 Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly
280 50 55
283 <210> SEQ ID NO: 9
284 <211> LENGTH: 41
285 <212> TYPE: PRT
286 <213> ORGANISM: Bos taurus
288 <400> SEQUENCE: 9
289 Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu
290 1 5 10 15
291 Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala
292 20 25 30
293 Asn Ile Thr Ile Val Glu Ser Asn Ala
294 35 40
297 <210> SEQ ID NO: 10
298 <211> LENGTH: 122
299 <212> TYPE: DNA
300 <213> ORGANISM: Bos taurus
302 <220> FEATURE:
303 <221> NAME/KEY: CDS
304 <222> LOCATION: (2)...(122)
306 <400> SEQUENCE: 10
307 g aag tca gaa ctt cgc att agc aaa gcg tca ctg gct gat tct gga gaa 49
308 Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu
309 1 5 10 15
311 tat atg tgc aaa gtg atc agc aaa cta gga aat gac agt gcc tct gcc 97

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/530,884A

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Input Set : A:\PTO.AMC.TXT
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:46; N Pos. 214
Seq#:51; N Pos. 895